

TTCTATCGAT	TGAATTC	CCCC	GGGGATC	CCTC	TAGAGAT	CCCC	TCGAC	CCTCGA						50
CCCACGCGTC	CGCCGGG	CGG	CGGCTTT	TGGA	TTTTG	GGGGGG	GCGGGG	ACCA						100
GCTGCGCGGC	GGCACC		ATG	TTC	CTA	GCC	ACT	CTG	TAC	TTC				140
			Met	Phe	Leu	Ala	Thr	Leu	Tyr	Phe				
			1				5							
GCG	CTG	CCA	CTC	CTG	GAT	TTG	CTG	ATG	TCC	GCC	GAG	GTG		179
Ala	Leu	Pro	Leu	Leu	Asp	Leu	Leu	Met	Ser	Ala	Glu	Val		
	10					15					20			
AGT	GGT	GGA	GAC	CGT	CTG	GAC	TGT	GTG	AAA	GCC	AGC	GAT		218
Ser	Gly	Gly	Asp	Arg	Leu	Asp	Cys	Val	Lys	Ala	Ser	Asp		
			25				30							
CAG	TGC	CTG	AAG	GAA	CAG	AGC	TGC	AGC	ACC	AAG	TAC	CGC		257
Gln	Cys	Leu	Lys	Glu	Gln	Ser	Cys	Ser	Thr	Lys	Tyr	Arg		
	35				40					45				
ACA	CTA	AGG	CAG	TGC	GTG	GCG	GGC	AAG	GAA	ACC	AAC	TTC		296
Thr	Leu	Arg	Gln	Cys	Val	Ala	Gly	Lys	Glu	Thr	Asn	Phe		
		50					55					60		
AGC	CTG	ACA	TCC	GGC	CTT	GAG	GCC	AAG	GAT	GAG	TGC	CGT		335
Ser	Leu	Thr	Ser	Gly	Leu	Glu	Ala	Lys	Asp	Glu	Cys	Arg		
				65					70					
AGC	GCC	ATG	GAG	GCC	TTG	AAG	CAG	AAG	TCT	CTG	TAC	AAC		374
Ser	Ala	Met	Glu	Ala	Leu	Lys	Gln	Lys	Ser	Leu	Tyr	Asn		
	75					80					85			
TGC	CGC	TGC	AAG	CGG	GGC	ATG	AAG	AAA	GAG	AAG	AAT	TGT		413
Cys	Arg	Cys	Lys	Arg	Gly	Met	Lys	Lys	Glu	Lys	Asn	Cys		
			90					95						
CTG	CGT	ATC	TAC	TGG	AGC	ATG	TAC	CAG	AGC	CTG	CAG	GGA		452
Leu	Arg	Ile	Tyr	Trp	Ser	Met	Tyr	Gln	Ser	Leu	Gln	Gly		
100					105					110				
AAT	GAC	CTC	CTG	GAA	GAT	TCC	CCG	TAT	GAG	CCG	GTT	AAC		491
Asn	Asp	Leu	Leu	Glu	Asp	Ser	Pro	Tyr	Glu	Pro	Val	Asn		
		115					120					125		

FIG. 1A





CAC CTC TGT CTT TCT GAT AGT GAT TTC GGA AAG GAT GGT	1388
His Leu Cys Leu Ser Asp Ser Asp Phe Gly Lys Asp Gly	
415 420	
CTC GCT GGT GCC TCC AGC CAC ATA ACC ACA AAA TCA ATG	1427
Leu Ala Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met	
425 430 435	
GCT GCT CCT CCC AGC TGC AGT CTG AGC TCA CTG CCG GTG	1466
Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu Pro Val	
440 445 450	
CTG ATG CTC ACC GCC CTT GCT GCC CTG TTA TCT GTA TCG	1505
Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser	
455 460	
TTG GCA GAA ACG TCG TAGCTGCATC CGGGAAAACA GTATGAAAAG	1550
Leu Ala Glu Thr Ser	
465 468	
ACAAAAGAGA ACCAAGTATT CTGTCCCTGT CCTCTTGTAT ATCTGAAAAT	1600
CCAGTTTAA AAGCTCCGTT GAGAAGCAGT TTCACCCAAC TGGAACCTTT	1650
TCCTTGTTTT TAAGAAAGCT TGTGGCCCTC AGGGGCTTCT GTTGAAGAAC	1700
TGCTACAGGG CTAATTCCAA ACCCATAAGG CTCTGGGGCG TGGTGCGGCT	1750
TAAGGGGACC ATTTGCACCA TGTAAGCAA GCTGGGCTTA TCATGTGTTT	1800
GATGGTGAGG ATGGTAGTGG TGATGATGAT GGTAAATTTA ACAGCTTGAA	1850
CCCTGTTCTC TCTACTGGTT AGGAACAGGA GATACTATTG ATAAAGATTC	1900
TTCCATGTCT TACTCAGCAG CATTGCCTTC TGAAGACAGG CCCGCAGCCT	1950
AGTGTGAATG ACAAGTGGAG GTTGGCCTCA AGAGTGGACT TGGCAGACTC	2000
TACCTTGTAG TAATGTTTAC CTTTCCGTGT ATGGTCTCCA CAGAGTGTTT	2050
ATGTATTTAC AGACTGTTCT GTGATCCCCC AACAACAACA ACCACAAATT	2100
CCTTGGTCAC CTCCAAATGT AACCGGTCCT TTAGCCCAGT AGAGGAGGGT	2150
GGGTGTGGCC CTGGCACAGC TCCCGGATTG TTGATGGGCA CTCTCCTGAG	2200

FIG. 1D

CTTTGCTTGA	GTGAGAAGCT	GAATGTAGCT	GAAAATCAAC	TCTTCTTACA	2250
CTTAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	2300
AAAAAAAAAA	AAAAGGTTTA	GGGATAACAG	GGTAATGCGG	CCGCGTCGAC	2350
CTGCAGAAGC	TTGGCCGCCA	TGGCCCAA			2378

**FIG. 1E**

↓  
MELATLYFALPLLDLLMSAEVSGGDRLDCVKASDQCLKEQCSTKYRTLRQCVAGKETNE  
SLTSGLEAKDECRSAMEALKQKSLYNCRCKRGMKEKNCLRIYWSMYQSLQGNDLLEDSP  
YEPVNSRLSDIFRAVPFISDVFQQVEHISKGNCLDAAKACNLDDTCKKYRSAYITPCTT  
SMSNEVCNRRKCHKALRQFFDKVPAKHSYGMLFCSCRDIACTERRRRQTIVPVCSYEER  
PNCLSLQDSCKTNYICRSRLADFFTNCQPESRSVSNCLNENYADCLLAYSGLIGTVMTPN  
YVDSSSLSVAPWCDCSNSGNDLEDCLKFLNFFKDNTCLKNAIQAFGNGSDVTMWQPAPPV  
QTTTATTTAFRVKNKPLGPAGSENEIPTHVLPPCANLQAQKLKSNVSGSTHLCLSDSDF  
GKDGLAGASSHITTKSMAAPPSCSLSSLPVLMLTALAALLSVSLAETS

FIG. 2

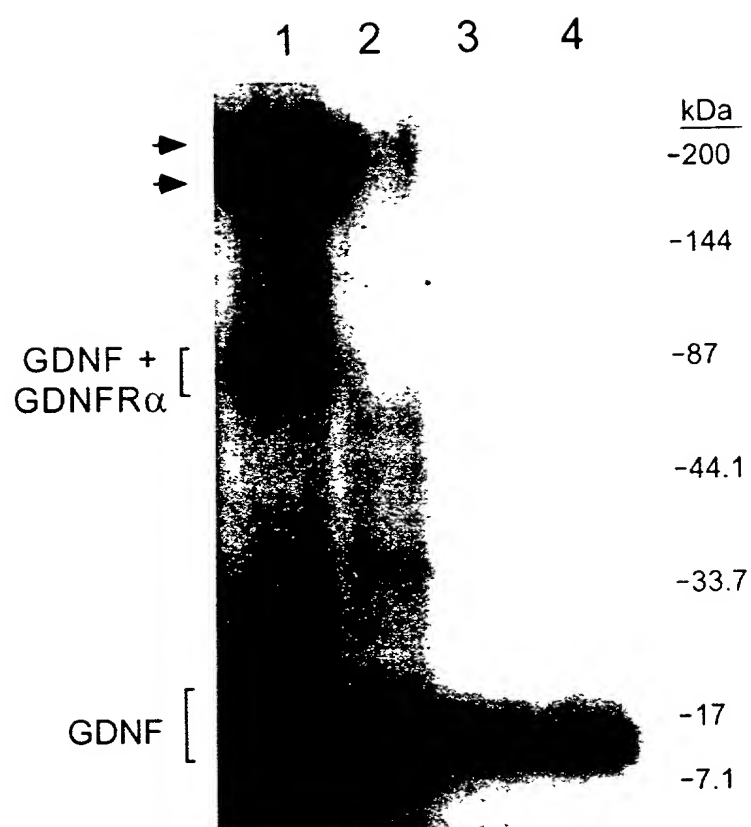


FIG. 3

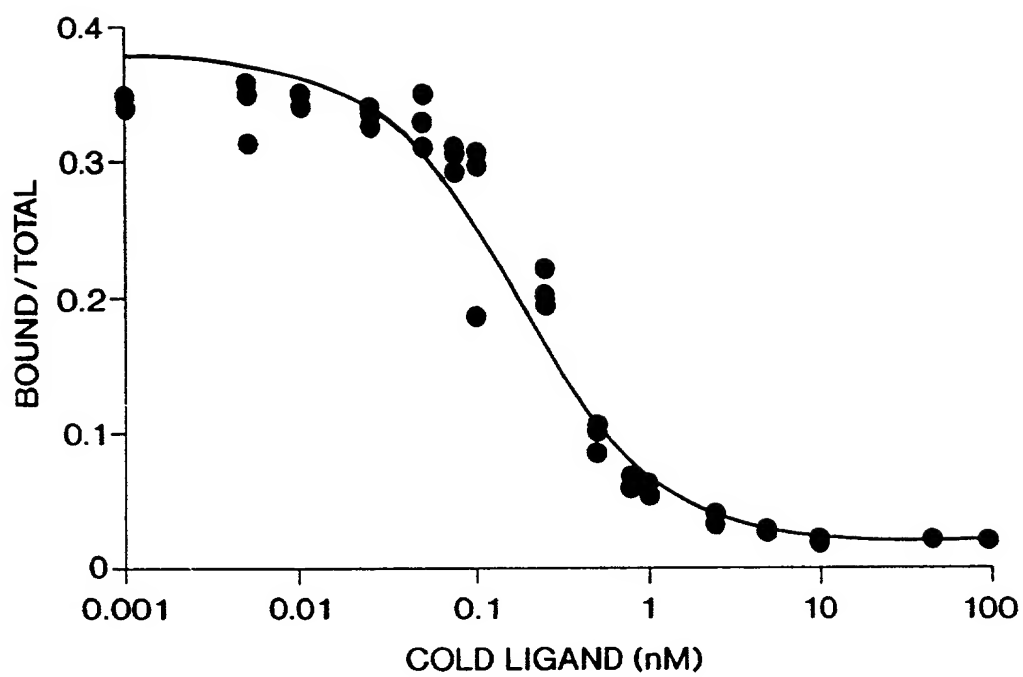


FIG. 4A

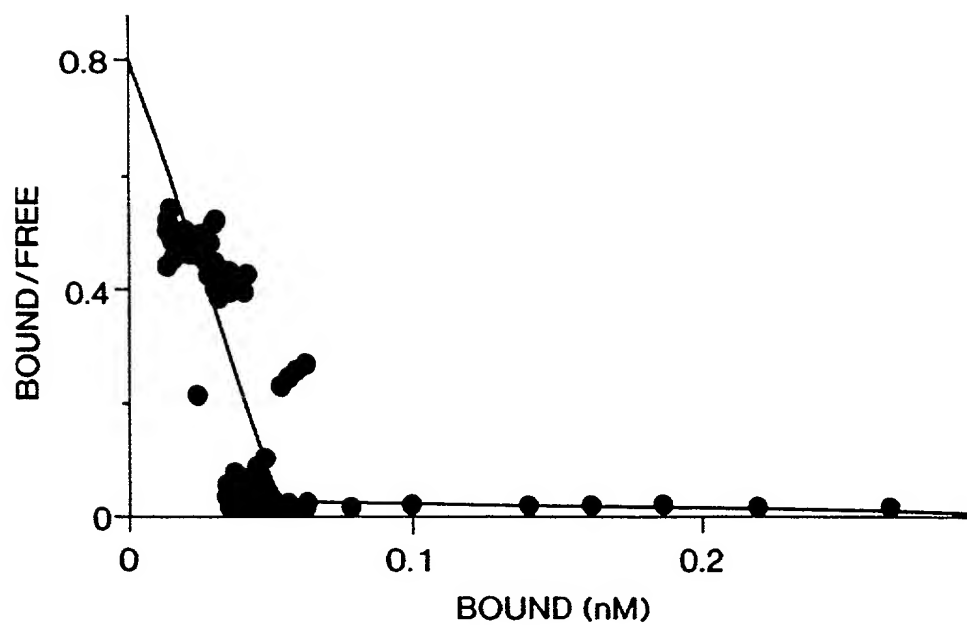


FIG. 4B



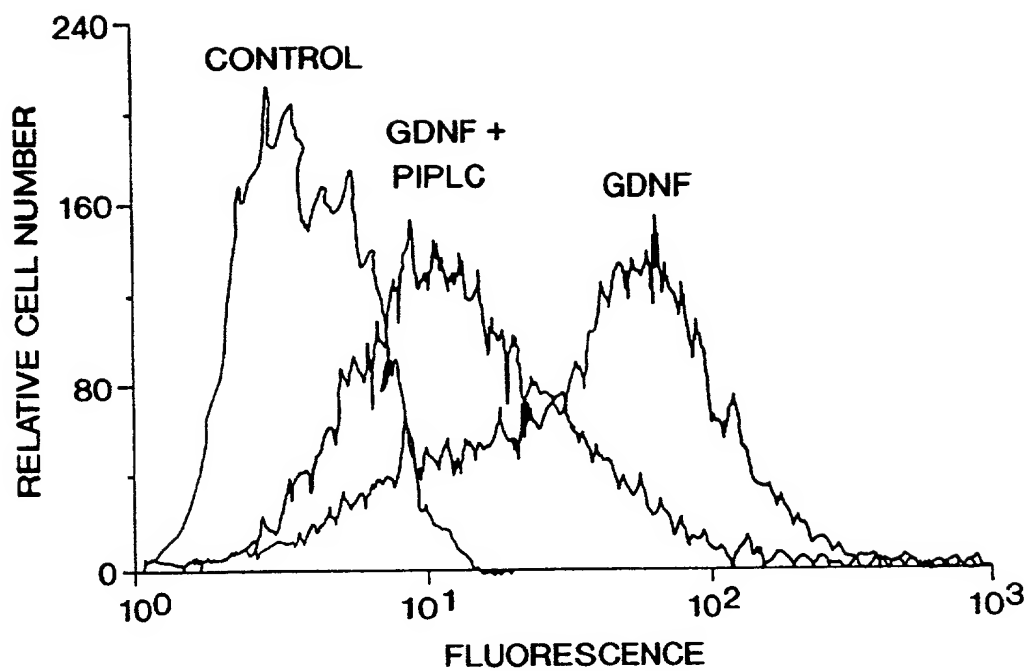


FIG. 5

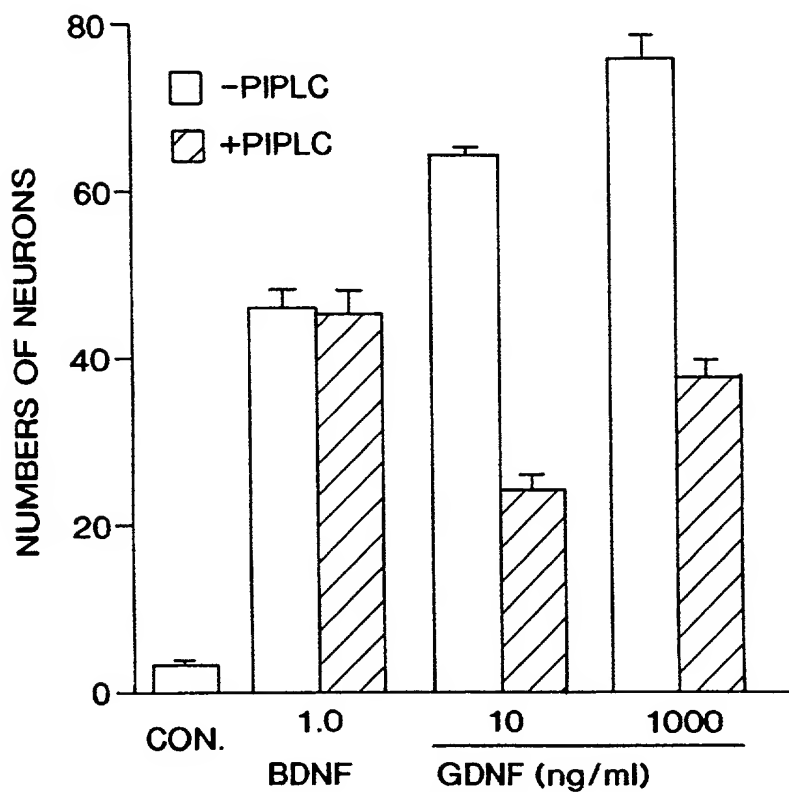


FIG. 6

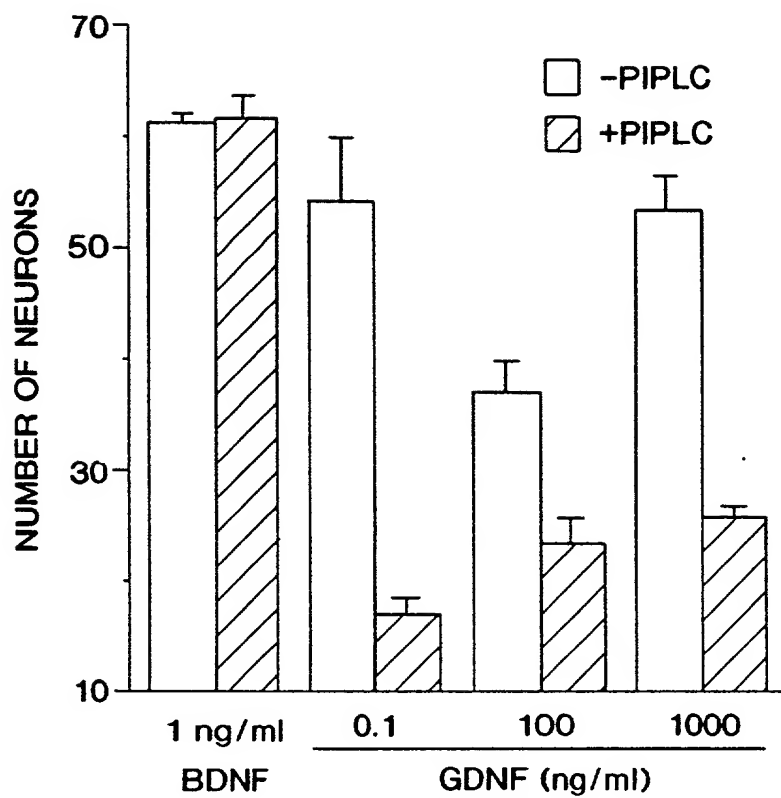


FIG. 7

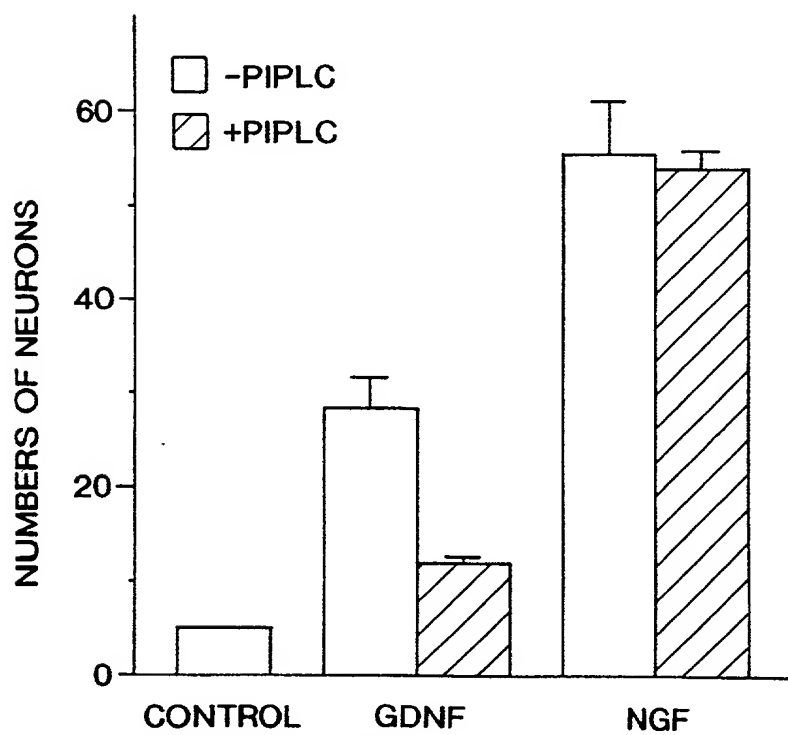
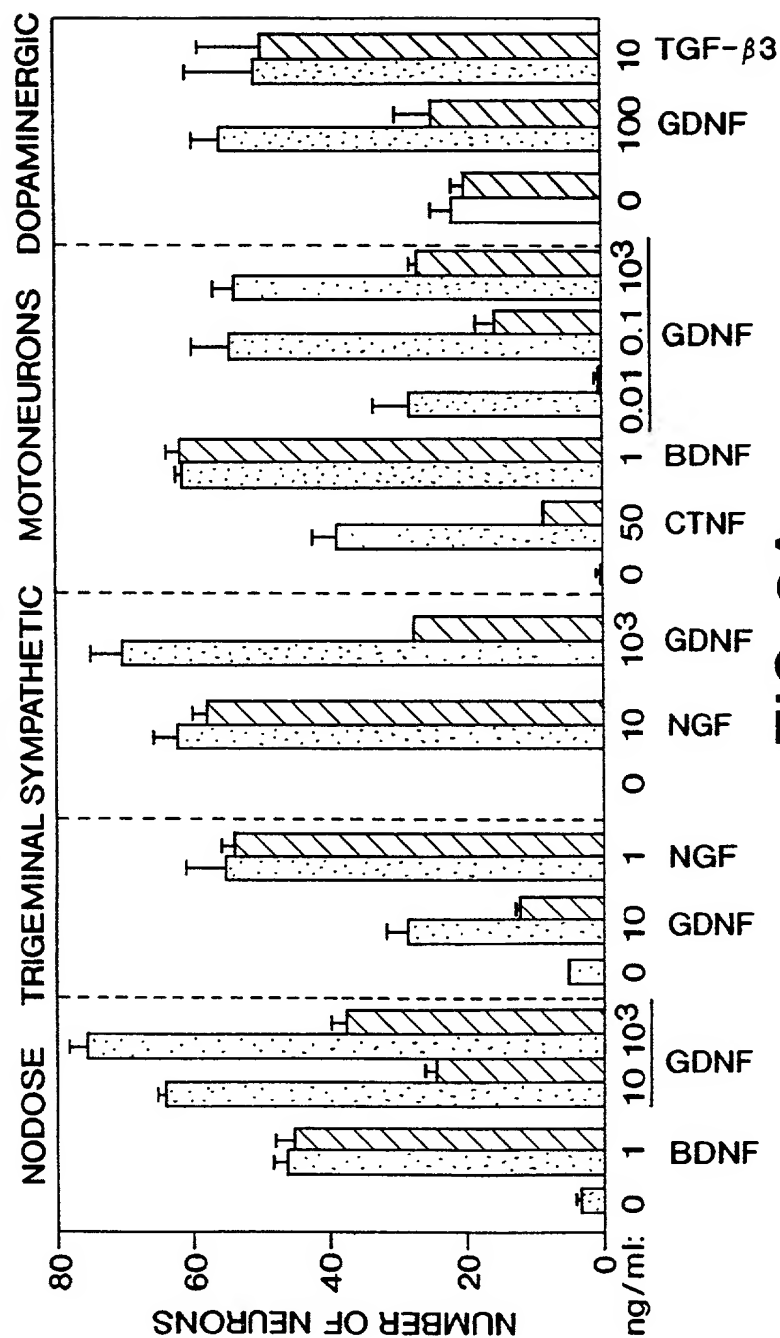


FIG. 8



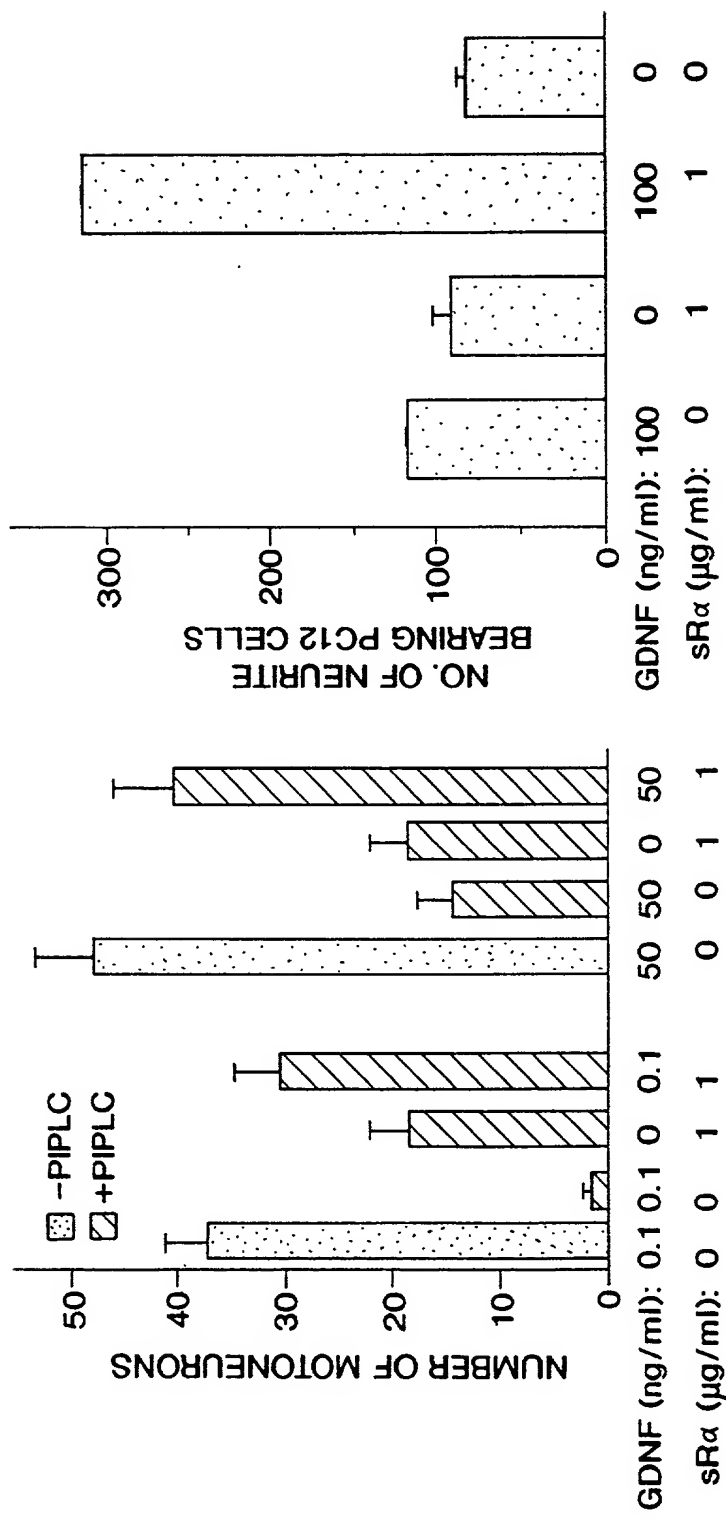


FIG. 9C

FIG. 9B

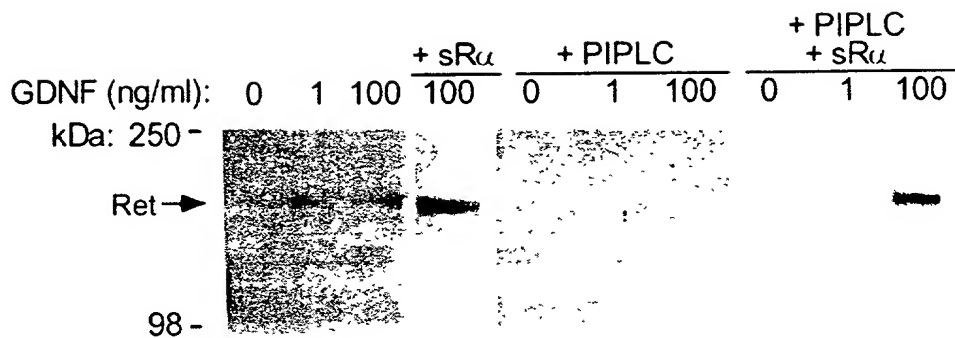


FIG. 10A

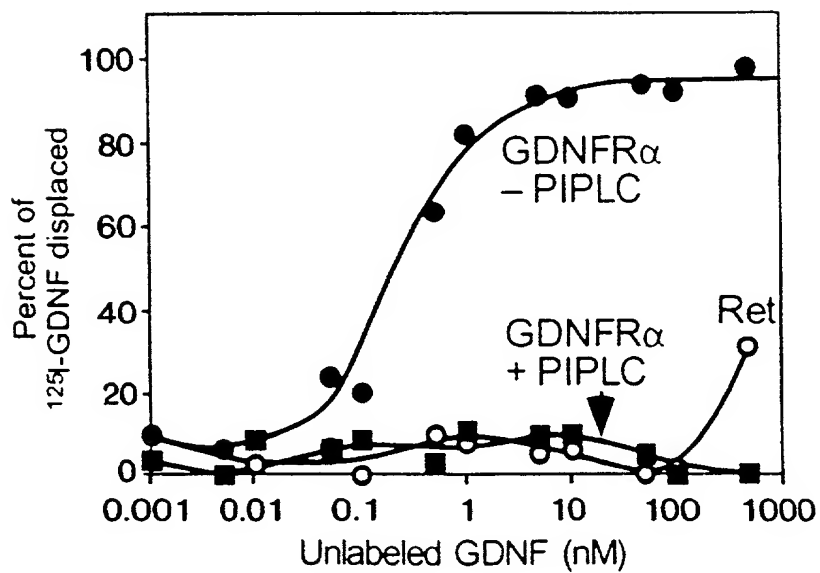


FIG. 10B

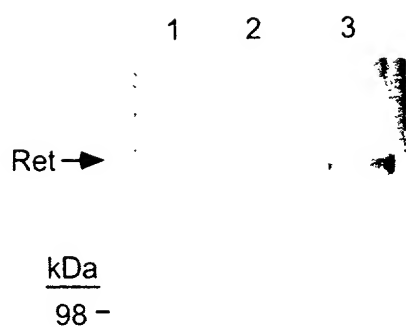


FIG. 10C

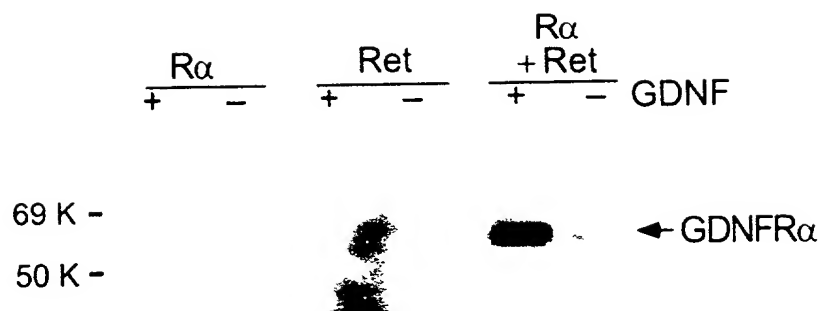


FIG. 10D